

OM protein - nucleic search, using frame_plus_pzn model

Run on: November 11, 2005, 20:16:49 ; Search time 3276 Seconds

(without alignments)
6146.520 Million cell updates/sec

Title: US-10-628-432-32

Perfect score: 2859

Sequence: 1 MSQSGSHRGRLAGKWLWGA.....DQLQDFNIPQAVYKDDDK 529

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=EST -OPMT=fastap -SUFFIX=err -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTFMT=pct -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database:

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3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2805	98.1	2514	9	AY404850 Homo sapi
2	2774	97.0	2514	9	AY404851 Pan trogl
3	2460	86.0	3673	3	AK083534 Mus muscu
4	2459	86.0	2502	9	AY404852 Mus muscu
5	2447	85.6	4390	3	AK028364 Mus muscu
6	1638	57.3	3025	3	AK076295 Mus muscu
7	1362.5	47.7	845	6	CD619814 Mus muscu
8	1223	42.8	2931	3	BC003269 Mus muscu
9	1170	40.9	827	6	CD619810 Mus muscu

C	10	1154	40.4	827	6	CD619812	CD619812 560703433
	11	1113	38.9	848	6	CB321525	CB321525 AGENCOURT
	12	1025	35.9	651	6	BY753951	BY753951 BY753951
C	13	1008	35.3	598	4	BM069515	BM069515 1e8909.x
	14	1003	33.1	681	2	BE912007	BE912007 601662774
	15	952	33.3	590	6	CD619809	CD619809 560703354
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	20	854.5	29.9	932	6	CA788933	CA788933 AGENCOURT
	21	841	29.4	736	7	CF734236	CF734236 UI-M-HBO
	22	835	29.2	531	9	CG549416	CG549416 OST152925
C	23	824.5	28.8	551	6	CB614460	CB614460 AMGNNUC:N
	24	810	28.3	643	3	CB619813	CB619813 56070459H
	25	806	28.2	719	5	BU701949	BU701949 UI-M-FIO
	26	786	27.5	520	9	CG633232	CG633232 OST152674
	27	772.5	27.0	769	7	CO432359	CO432359 UI-M-HBO
	28	760	26.6	1930	3	AK090358	AK090358 Mus muscu
	29	756.5	26.5	788	7	CR629695	CR629695 DKF2p469L
	30	738.5	25.8	664	7	CF170010	CF170010 B0821D01-
	31	736.5	25.8	595	6	CD623530	CD623530 56035048H
	32	734.5	25.7	743	7	CF741826	CF741826 UI-M-HBO
	33	719	25.1	692	7	CN459174	CN459174 UI-M-HBO
	34	709.5	24.8	580	7	CF168714	CF168714 B0803E12-
	35	709	24.8	421	5	BY218603	BY218603 BY218603
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	37	697.5	24.4	502	5	BP293170	BP293170 BP293170
	38	685	24.0	3583	3	AK043875	AK043875 Mus muscu
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C	40	683	23.9	440	2	BF850604	BF850604 PM1-EN006
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	42	663.5	23.2	580	5	BP378639	BP378639 BP378639
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	44	663	23.2	799	7	CO247237	CO247237 AGENCOURT
	45	656	22.9	849	7	CO247095	CO247095 AGENCOURT

ALIGNMENTS

RESULT 1	AY404850	2514 bp	DNA	linear	GSS 16-DEC-2003
LOCUS	AY404850				
DEFINITION	Homo sapiens ADAMTS4 gene, VIRTUAL TRANSCRIPT, partial sequence,				
ACCESSION	AY404850				
VERSION	AY404850.1	GI.39760827			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarwal,A., Mammalia,Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 2514)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 2514)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Substitution				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
source	1..2514				

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 11, 2005, 20:28:25 ; Search time 806 Seconds
(without alignments)
5427.710 Million cell updates/sec

Title: US-10-628-432-32
Perfect score: 2859
Sequence: 1 MSOTGSHRGRLAGRLWGA.....DQLDFNIPQAVDYKDDDK 529

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9794790 seqs, 413490567 residues
Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2805	98.1	4192	16 US-10-247-685-1	Sequence 1, Appli
2	2804	98.1	2542	20 US-10-628-432-14	Sequence 14, Appli
3	2801	98.0	1561	19 US-10-358-283-33	Sequence 33, Appli
4	2801	98.0	1726	19 US-10-358-283-32	Sequence 32, Appli
5	2801	98.0	4307	18 US-10-191-997-121	Sequence 121, Appli
6	2801	98.0	4307	19 US-10-358-283-31	Sequence 31, Appli
7	2801	98.0	4307	20 US-10-628-432-4	Sequence 4, Appli
8	2801	98.0	4307	22 US-10-946-374-316	Sequence 173, Appli
9	2798	97.9	4407	10 US-10-052-586-351	Sequence 316, Appli
10	2798	97.9	4407	14 US-10-176-758-351	Sequence 351, Appli
11	2798	97.9	4407	15 US-10-176-758-351	Sequence 351, Appli
12	2798	97.9	4407	15 US-10-176-758-351	Sequence 351, Appli
13	2798	97.9	4407	15 US-10-176-758-351	Sequence 351, Appli
14	2798	97.9	4407	15 US-10-176-758-351	Sequence 351, Appli
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16	2798	97.9	4407	15 US-10-176-758-351	Sequence 351, Appli
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18	2798	97.9	4407	15 US-10-176-758-351	Sequence 351, Appli
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20	2798	97.9	4407	15 US-10-176-758-351	Sequence 351, Appli
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29	2798	97.9	4407	15 US-10-176-758-351	Sequence 351, Appli
30	2798	97.9	4407	15 US-10-176-758-351	Sequence 351, Appli
31	2798	97.9	4407	15 US-10-176-758-351	Sequence 351, Appli
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42	2798	97.9	4407	15 US-10-176-758-351	Sequence 351, Appli
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44	2798	97.9	4407	15 US-10-176-758-351	Sequence 351, Appli
45	2798	97.9	4407	15 US-10-176-758-351	Sequence 351, Appli

ALIGNMENTS

RESULT 1
US-10-247-685-1
Sequence 1, Application US/10247685
Publication No. US20030108998A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FILE REFERENCE: DM6909D
CURRENT APPLICATION NUMBER: US/10/247,685
CURRENT FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 4192

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 11, 2005, 20:27:24 ; Search time 194 Seconds

(without alignments)
4461.806 Million cell updates/sec

Title: US-10-628-432-32

Sequence: 1 MSQSHRGRGLAGRWLWGA.....DQLQDFNIPQAVDYKDDDK 529

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=x1h
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blowm62 -TRANS=human40.cdi
-LIST=5 -POCALIGN=200 -THR_SCORE=DCT -THR_MAX=100 -THR_MIN=0 -ALIGN=20
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Database: Issued_Patents_NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2805	98.1	4192	3	US-09-122-126B-1
2	2805	98.1	4192	3	US-09-634-286A-1
3	2805	98.1	4192	4	US-10-247-685-1
4	1193	41.7	4676	3	US-09-130-491-1
5	1189	41.6	3889	4	US-09-568-559-1
6	1180	41.3	4858	3	US-09-392-184-1
7	1097	38.4	2853	4	US-10-009-332-2
8	1055	36.9	3706	3	US-09-484-970B-58
9	1050	36.7	2184	4	US-09-445-023A-13
10	1046.5	36.6	3618	4	US-09-445-023A-13
11	1011.5	35.4	3638	4	US-09-369-364A-8
12	870	30.4	3126	3	US-09-392-184-7

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14	828	29.0	3250	3	US-09-122-126B-1	Sequence 14, Appl
15	828	29.0	3250	4	US-09-634-286A-14	Sequence 14, Appl
16	828	29.0	3250	4	US-10-247-685-14	Sequence 14, Appl
17	783.5	27.4	5804	3	US-09-369-364A-12	Sequence 12, Appl
18	733	25.6	2625	3	US-09-369-364A-14	Sequence 14, Appl
19	717	25.1	6659	3	US-09-321-987B-1	Sequence 1, Appl
20	645.5	22.6	3918	4	US-09-369-364A-6	Sequence 6, Appl
21	643.5	22.5	5357	3	US-09-392-184-5	Sequence 5, Appl
22	636	22.2	1730	3	US-09-369-364A-10	Sequence 10, Appl
23	592	20.7	2727	4	US-09-963-791-11	Sequence 11, Appl
24	592	20.7	2727	4	US-09-963-791-11	Sequence 11, Appl
25	578.5	20.2	3571	4	US-09-799-451-411	Sequence 1, Appl
26	574	20.1	3377	4	US-09-981-953A-3	Sequence 3, Appl
27	570	19.9	703	3	US-09-392-184-6	Sequence 3, Appl
28	559.5	19.6	1317	4	US-09-963-791-21	Sequence 21, Appl
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30	556.5	19.5	3766	4	US-09-981-953A-1	Sequence 1, Appl
31	544.5	19.0	1524	4	US-09-963-791-9	Sequence 9, Appl
32	515.5	18.0	4042	3	US-09-930-872-5	Sequence 5, Appl
33	515.5	18.0	4042	4	US-10-217-774-3	Sequence 3, Appl
34	512	17.9	1071	4	US-09-963-791-19	Sequence 19, Appl
35	505.5	17.7	3675	3	US-09-930-872-3	Sequence 3, Appl
36	505.5	17.7	3675	4	US-10-217-774-3	Sequence 3, Appl
37	486.5	17.0	2450	3	US-09-491-532-2	Sequence 2, Appl
38	486.5	17.0	6692	3	US-09-491-532-1	Sequence 1, Appl
39	486.5	17.0	3636	4	US-09-949-016-5530	Sequence 25, Appl
40	482.5	16.9	3160	4	US-09-963-791-25	Sequence 8, Appl
41	479.5	16.8	2450	3	US-09-491-532-9	Sequence 16, Appl
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43	472	16.5	3885	3	US-09-369-364A-16	Sequence 1139, Ap
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ALIGNMENTS

RESULT 1
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Sequence 1, Application US/09122126B
Patent No. 6451575
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FILE REFERENCE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,126B
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 4192

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (406)..(2916)
US-09-122-126B-1

Alignment Scores:

Pred. No.: 8.58e-239
Score: 2805.00
Percent Similarity: 100.00%
Best Local Similarity: 99.81%
Query Match: 98.11%
DB: 3
Gaps: 0

US-10-628-432-32 (1-529) x US-09-122-126B-1 (1-4192)

QY 1 MetSerGlnThrGlySerHisProGlyArgGlyLeuAlaGlyArgTrpLeuTrpGlyAla 20
DB 406 ATGTCCCAACAGCGCTCGCATCCGGAGAGGGCTTGCGAGGGCTGCTGGGAGCC 465
QY 21 GlnProCysLeuLeuLeuProIleValProLeuSerTrpLeuValTrpLeuLeuLeu 40

GenCore version 5.1.6
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Om protein - nucleic search, using frame_plus_p2n model

Run on: November 11, 2005, 19:59:59 ; Search time 555 Seconds

(without alignments)
5642.420 Million cell updates/sec

Title: US-10-628-432-32

Perfect score: 2859
Sequence: 1 MSQTGSHPGKGLAGRLMGA.....DQLDFNIPQAVDYDDDDK 529

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-Q/cgml_1/USPTO.spool/US10628432/runat 03112005 080225 14117/app query.fasta_1.711
-DB=N_Geneseq 16Dec04 -QPM=fastcap -SUFFIX=mg -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10628432 @CGML 1 1 470 @runat 03112005 080225 14117 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq 16Dec04:*

1: geneseqn1980s:*\n2: geneseqn1990s:*\n3: geneseqn2000s:*\n4: geneseqn2001as:*\n5: geneseqn2001bs:*\n6: geneseqn2002as:*\n7: geneseqn2002bs:*\n8: geneseqn2003as:*\n9: geneseqn2003bs:*\n10: geneseqn2003cs:*\n11: geneseqn2003ds:*\n12: geneseqn2004as:*\n13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2805	98.1	4192	2	AAx00725
2	2804	98.1	2542	13	ADs20217
3	2801	98.0	1560	10	ADb85506
4	2801	98.0	1725	10	ADb85505
5	2801	98.0	2514	10	ADL13488
					ADL13488 Osteocarth

6	2801	98.0	4301	4	AA168146	AA168146 Human agg
7	2801	98.0	4301	10	ADL13487	ADL13487 Osteocarth
8	2801	98.0	4303	3	AAa95826	AAa95826 Human met
9	2801	98.0	4307	10	ADb85504	ADb85504 Human agg
10	2801	98.0	4307	10	ACF63399	ACF63399 Human ADa
11	2801	98.0	4307	13	ADs20212	ADs20212 Human ADa
12	2798	97.9	4406	4	AAa46100	AAa46100 Human DNA
13	2798	97.9	4407	3	AAa37111	AAa37111 Human DNA
14	2798	97.9	4407	4	AAa54426	AAa54426 Human PRO
15	2798	97.9	4407	4	ACA89550	ACA89550 CDNA enco
16	2798	97.9	4407	8	ACA73560	ACA73560 CDNA enco
17	2798	97.9	4407	8	ACA05875	ACA05875 Human sec
18	2798	97.9	4407	8	ACA66709	ACA66709 CDNA enco
19	2798	97.9	4407	8	ACF20284	ACF20284 Human sec
20	2798	97.9	4407	8	ACF19670	ACF19670 Human sec
21	2798	97.9	4407	8	ACD21958	ACD21958 Human sec
22	2798	97.9	4407	8	ACF13123	ACF13123 Human sec
23	2798	97.9	4407	8	ACD25226	ACD25226 Human sec
24	2798	97.9	4407	8	ACF00275	ACF00275 Human sec
25	2798	97.9	4407	8	ACA72332	ACA72332 Human sec
26	2798	97.9	4407	8	ACD04856	ACD04856 Human sec
27	2798	97.9	4407	8	ACD18317	ACD18317 Human sec
28	2798	97.9	4407	8	ACA88758	ACA88758 Human sec
29	2798	97.9	4407	8	ACA88758	ACA88758 Human sec
30	2798	97.9	4407	8	ACA70200	ACA70200 Human sec
31	2798	97.9	4407	8	ACD12422	ACD12422 Human sec
32	2798	97.9	4407	8	ACD74337	ACD74337 Human sec
33	2798	97.9	4407	8	ACD15965	ACD15965 Human sec
34	2798	97.9	4407	8	ACD25533	ACD25533 Human sec
35	2798	97.9	4407	8	ACD18010	ACD18010 Human sec
36	2798	97.9	4407	8	ACD88297	ACD88297 Human sec
37	2798	97.9	4407	8	ACD21651	ACD21651 Human sec
38	2798	97.9	4407	8	ACD18718	ACD18718 Human sec
39	2798	97.9	4407	8	ABX98328	ABX98328 Human sec
40	2798	97.9	4407	8	ACD14079	ACD14079 Human PRO
41	2798	97.9	4407	8	ACD09859	ACD09859 Human sec
42	2798	97.9	4407	8	ACD88604	ACD88604 Human sec
43	2798	97.9	4407	8	ACD21344	ACD21344 Human sec
44	2798	97.9	4407	8	ABX75716	ABX75716 Human sec
45	2798	97.9	4407	8	ABX97919	ABX97919 Human PRO

ALIGNMENTS

RESULT 1
AAx00725
ID AAx00725 standard; cDNA to mRNA; 4192 BP.

AC AAx00725;

DT 30-MAR-1999 (first entry)

DE Human aggrecan degrading metalloprotease 1 gene.

KW Human; aggrecan degrading metalloprotease; cartilage; proteoglycan;
KW interglobular domain; matrix metalloprotease; bovine; interleukin-1beta;
KW primer; PCR; amplification; inhibitor; cleavage; inhibitor; ADMP; ss;
KW arthritis; joint injury; pseudogout.

OS Homo sapiens.

FT Key Location/Qualifiers
FT CDS 406..2919
FT /tag= a
FT /product= "ADMP-1"

FT /note= "aggrecan degrading metalloprotease 1"

PN MO9905291-A2.

PD 04-FEB-1999.

PP 24-JUL-1998; 98WO-US015438.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 11, 2005, 20:15:59 ; Search time 4498 Seconds
(without alignments)

5698.713 Million cell updates/sec

Title: US-10-628-432-32

Sequence: 1 MSQTSHPGRGLAGRWLWCA.....DQLQDPNIPQAVDYKDDDDK 529

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 2422767955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing filter 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgm2_1/USPFO.epool/US10628432/runat_03112005_080225_14127/app.query.fasta_1.711
-DB=genembl -QMT=faeap -SUFFIX=rge -MINMATCH=0.1 -LOOFC=0 -LOOEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blomsu62 -TRANS=humand0.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pcit -THR MAX=100 -THR MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USBR=US10628432 @CGN 1.1 3552 @runat_03112005_080225_14127 -NCPU=6 -ICPU=3
-NO MMAP -LARGEOBFRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
-DET TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Genembl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_dat:*
7: gb_dm:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sls:*
12: gb_gy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2805	98.1	4192	6	AR230264
2	2805	98.1	4192	6	AR282324
3	2805	98.1	4192	6	AR560177
4	2805	98.1	4192	6	BD073443

5	2805	98.1	4193	9	AF148213
6	2801	98.0	4301	6	BD016729
7	2801	98.0	4301	6	AB014588
8	2798	97.9	4407	6	AX376284
9	2798	97.9	4407	6	AX597248
10	2798	97.9	4407	6	AY358886
11	2790	97.6	4341	9	BC063293
12	2777	97.1	2317	6	CO716637
13	2557	89.4	3720	4	AF516915
14	2459	86.0	3321	10	BC027773
15	2427.5	84.9	4281	10	AK173001
16	2170	75.9	167863	2	AL590651
17	2151.5	75.3	133512	9	AL590714
18	2147.5	75.1	10766	9	AY044847
19	1830	64.0	11991	9	BC030812
20	1655.5	57.9	221776	10	AC084821
21	1655.5	57.9	221776	2	AC093409
22	1593	55.7	1251	10	AB042271
23	1593	55.7	1878	6	BD094440
24	1527	42.9	4180	6	BD129556
25	1227	42.9	4180	10	D67076
26	1223	42.8	3943	10	BC040382
27	1223	42.8	4909	10	BC050834
28	1222	42.7	2871	6	AX577901
29	1221.5	42.7	4878	10	AF149118
30	1220.5	42.7	4395	10	BC080237
31	1203	42.1	2857	10	AF304446
32	1193	41.7	2853	6	ES6656
33	1193	41.7	3261	6	BD129546
34	1193	41.7	3430	6	AX577976
35	1193	41.7	4014	6	AF060152
36	1193	41.7	4014	6	E29406
37	1193	41.7	4309	9	AB037767
38	1193	41.7	4665	9	BC036515
39	1193	41.7	4676	6	AR217550
40	1193	41.7	4676	6	BD080292
41	1191	41.7	4447	9	AF170084
42	1189	41.6	3889	6	AR430581
43	1189	41.6	4659	9	AF207664
44	1186.5	41.5	4666	9	HS080753
45	1181	41.3	4712	6	BD194902

ALIGNMENTS

RESULT 1	AR230264	Sequence 1 from patent US 6451575.	4192 bp	DNA	Linear	PAT 20-DEC-2002
LOCUS	AR230264					
DEFINITION	AR230264					
ACCESSION	AR230264					
VERSION	AR230264.1	GI:27270379				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 4192)					
AUTHORS	Arner,B.C., Burn,T.C., Copeland,R.A., Decicco,C.P., Liu,R., Magolda,R., Pratta,M., Solomon,K.A., Tortorella,M.D., Tzabkos,J.M. and Yang,F.					

TITLE AggreCan degrading metallo proteases
JOURNAL Patent: US 6451575-A 1 17-SEP-2002;
FEATURES Location/Qualifiers
source 1. 4192
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 7.76e-134
Score: 2805.00
Percent Similarity: 100.00%
Best Local Similarity: 99.81%
Query Match: 98.11%
Length: 4192
Matches: 519
Conservative: 1
Mismatch: 0
Indels: 0